Journal of Forestry Research (2012) 23(2): 285–288
DOI 10.1007/s11676-011-0215-3

ORIGINAL PAPER

Genetic divergence for growth and wood parameters in different clones of *Dalbergia sissoo* Roxb

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Received: 2010-11-29; Accepted: 2011-01-30

Abstract: The wood analysis for different parameters was carried out in a clonal seed orchard of *Dalbergia sissoo* Roxb. established during 1997 at Hoshiarpur, Punjab, India. Twelve clones with higher index value were subjected to Euclidean Cluster Analysis based on wood and growth parameters to group into seven clusters. Cluster I and II contained four and three clones, respectively, and remaining clusters had just one clone each. Clone originated from Barielly, Uttar Pradesh of cluster VII was found to be the most divergent clone. Cluster II with three clones maintained greater inter-cluster distance with other clusters. The divergence analysis has confirmed that the clones planted in the clonal seed orchard are sufficiently divergent and seed harvested from the orchard would maintain high diversity.

Keywords: *Dalbergia sissoo* Roxb.; seed orchard; wood and growth traits; genetic divergence; hybridization

Introduction

Dalbergia is a pantropical genus with more than 100 species distributed in tropical Asia, America and Australia. Twenty seven species of the genus are represented in India, of which 15 are indigenous. In fact, three of the species *viz*. *Dalbergia congesta, Dalbergia gardneriana* and *Dalbergis wattii* are endemic (Thothathri 1987). *Dalbergia sissoo* Roxb. (Shisham) is known internationally for its timber qualities. It is one of the fast growing tree species with a variety of adaptive and economic traits. The species is distributed between latitude 21°10′ N to 32°36′ N, longitude 74°48′ E to 93°26′ E and altitude up to 900 m in Sub-Himalayan tracts of India, occasionally ascending upto 1,000 m a.s.l. along the river and streams (Tewari 1994). It is very likely that Shisham is indigenous only to the Sub-Himalayan and Bhabar areas and has been introduced elsewhere (Troup 1921). Though the mature tree attains a maximum height of 30 m with diameter at breast height of 0.80 m under favorable conditions (Parrotta 1989), the trunks are often found to be crooked leading to higher degree of loses in the workshops (Tewari 1994).

The genetic improvement of this species has not been taken up in a systematic manner and only sporadic works are carried out mainly directed towards selection of plus trees and clonal propagation. In fact, there has absolutely been no published record on genetic improvement based on wood parameters, and only limited information is available about the degree of genetic variation or the heritability for wood traits. It is beyond doubt that genetics of wood traits is an essential aspect which becomes paramount important for a timber species like *D. sissoo*. Analysis of genetic diversity is one of the most important components for any of the breeding and genetic improvement programme which basically deals with ecosystem stability and forest sustainability (Libby 1973). The analysis of genetic diversity becomes still more valuable in tree improvement programme (Zobel 1971) owing to the long gestation period of trees. Obviously, analysis of genetic diversity enables selection of diverse parents for hybridization either to exploit the gain due to heterosis or synthesize new recombinants for subsequent generations. An attempt has been made to ascertain the magnitude of genetic diversity among the clones of *D. sissoo* using D^2 analysis. The present study was aimed to analyze the genetic diversity of various clones originated from different geographical regions.

Materials and methods

The wood material was collected from clonal seed orchard (CSO) established in 1996–1997, consisting of 27 clones selected from

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Responsible editor: Hu Yanbo

natural distribution range of Shisham of India and Nepal (Fig. 1). The clones were planted in randomized block design with a spacing of 5 m × 5 m at Punjab (altitude 267.30 m, altitude 31°31′36″N and longitude 75°48′54″E with rainfall of 1,242.20 mm) in an area of 2.40 ha. The CSO first recorded the growth traits including height, diameter at breast height (DBH), clear bole height (CBH)), straightness and branching behavior. Thereafter, the index values for individual ramets and clones were established, and a total of 12 clones with maximum index value were selected for the analysis of wood parameters. Further, two maximum scoring ramets of selected clones were marked in all the replications of CSO for analysis of wood parameters. A 5-mm thick increment borer was used for collecting wood samples at breast height (1.37 m), in this manner a total of 72 samples were collected. The cores were rubbed with formalin to prevent the fungal attack. Each core was divided into four equal segments from pith to periphery and named as pith, inner, middle and outer segments.

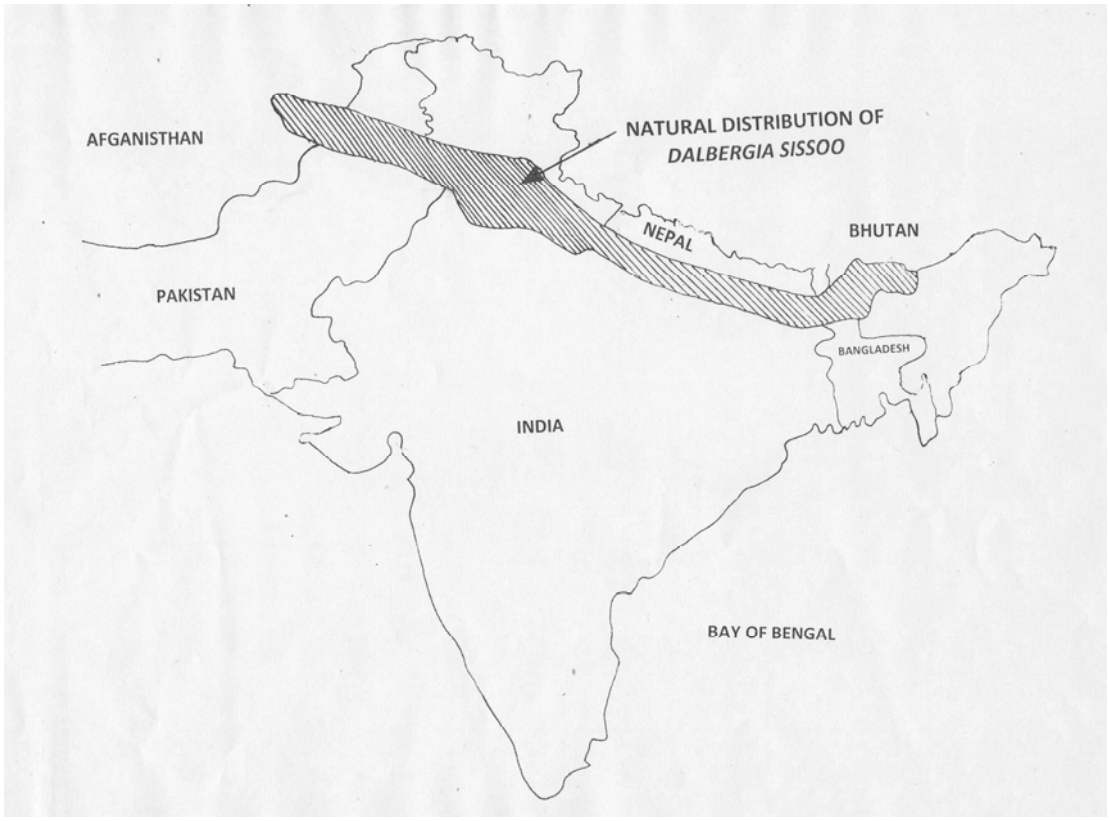

Fig. 1 Natural distribution range of *Dalbergia sissoo* Roxb in India.

In this way, a total of 288 samples were prepared for wood analysis and standard laboratory procedures were followed for micro-slides and macerations. The green volume of the samples was determined using water displacement method and the dry matter of the samples was calculated by oven drying at 103±2°C till constant weight. The specific gravity of different samples was accordingly calculated.

The radial cores were macerated with 50% nitric acid and a pinch of potassium chlorate as per Schultz's method. In fact, each core was individually dipped into test tubes filled with above mixture and kept in the sun light for maceration. The solution was decanted and washed several times with water to remove traces of acid and microscopic observations obtained. The average tangential diameter of the vessels was determined from 25 measurements and the same numbers of observations were recorded for various other parameters of the macerated wood for four locations *viz*. pith, inner, middle, and outer.

The growth and wood data were analyzed statistically as described by Sukhatame and Amble (1989) and D^2 analysis was performed using Mahalanobis's D^2 statistics (Mahalanobis 1936) using SAS (version 9.1.2 software for windows).

Results and discussion

Twelve clones of *D. sissoo* were grouped into seven clusters on the basis of Euclidean distances (Fig. 2). Cluster I consisted four clones (clones 41, 192, 33 and 57), cluster II three clones (Clone 2, 19 and 12) and rest of the clusters had one clone each (Table 1). The clustering indicates that though the species have sufficient genetic diversity, clones selected from the same geographical region come together in the same cluster (Table 1). All the clones of Cluster I and Cluster II are selected from the same geographical region of Pathri (except clone 192) and Bijnore, respectively. The position of clone 198 and clone 10 respectively in cluster III and VII again indicates that there is enough diver-

sity within the region as these clones tend to move to different clusters rather than group in clusters I and II. Similarly, clones selected from the geographical region of Gonda (232 and 204) were also grouped into two different clusters (Cluster V and VI). It is thus obvious that clones selected from a single region were spread over different clusters, which could probably be due to heterogeneity of genotypes, genetic architect of different genotypes, higher intensity of selection and high degree of general combining ability (Singh 2007).

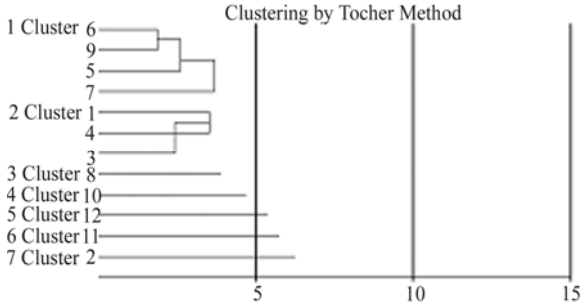

Fig. 2 Tocher method-based dendrogram

Table 1. Constituents of different clones and clusters

Cluster	S. No. (clone)	Origin
I	6 (41)	Pathri,Uttarakhand
	9 (192)	Saharanpur, Uttar Pradesh
	5 (33)	Pathri, Uttarakhand
	7 (57)	Pathri, Uttarakhand
II	1 (2)	Bijnore, Uttar Pradesh
	4 (19)	Bijnore, Uttar Pradesh
	3 (12)	Bijnore, Uttar Pradesh
III	8 (66)	Pathri, Uttarakhand
IV	10 (198)	Bareilly , Uttar Pradesh
V	12 (232)	Gonda , Uttar Pradesh
VI	11 (204)	Gonda , Uttar Pradesh
VII	2 (10)	Bijnore, Uttar Pradesh

Divergence analysis based on Mahalanobis D^2 statistics calculates degree of diversification and relative proportion of each component character to the total divergence among total individuals studied. It measures the forces of differentiation at two levels, *i.e*., at intra-cluster and inter cluster levels (Table 2). The intra-cluster distance ranged from 0.00 (cluster III, IV, V, VI and VII) to 4.06 (cluster I), indicating substantial diversity among the clones studied. The inter-cluster D^2 values ranged from 5.35 to 74.44. The D^2 value between cluster VII and VI (74.44) was the maximum, followed by between cluster VII and V (68.07), cluster VII and III (50.06), cluster VI and II (45.02) and cluster VII and I (43.89) (Table 2 and Fig 3). In fact, cluster VII (clone 10) showed maximum inter cluster distance from all other clusters (except cluster II) and the level of diversity was also substantially higher. Similar pattern of genetic diversity was observed in *Casuarina equisetifolia* (Kumar and Gurumurthi 2000). Singh (1993) explained that maximum heterosis occurs at an optimal or intermediate level of divergence. Besides the selection of divergent parents for hybridization and establishment of seed orchards, this technique measures the degree of diversification and determines the relative proportion of each component character to the total divergence. In forest tree crops, genetic divergence studies are also an effective tool for establishing seed orchards with diverse parents; so that improved seed in most economic manner is harvested as diverse parents would have equal opportunities for hybridization and production of quality seeds (Kumar and Gurumurthi 2000). Hybridization between the clones selected from diverse clusters is expected to express higher heterosis and produce desirable recombinants among the transgressive segregants (Dhillon et al. 2009). The technique has effectively been applied in various forest tree species to find out distinct populations / provenances / progenies in *Eucalyptus camaldulensis* (Burley et al. 1971; Andrew 1973) and *Acacia nilotica* (Bagchi 1992).

Table 2. Average inter- and intra-cluster distances in different clusters of *Dalbergia sissoo* (Mahalanobis Euclidean² Distances)*

Clusters	I	II	III	IV	V	VI	VII
I	**4.06**						
II	28.21	**3.61**					
III	6.26	29.69	**0.00**				
IV	9.82	24.00	8.47	**0.00**			
V	15.73	38.54	9.91	5.35	**0.00**		
VI	10.55	45.02	5.72	10.55	6.96	**0.00**	
VII	43.89	10.24	50.06	43.24	68.07	74.44	**0.00**

*Figure in bold indicate intra-cluster distance

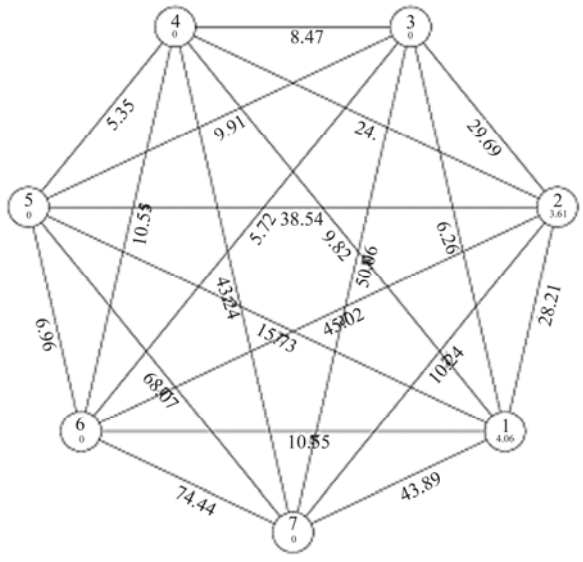

Fig 3. Mahalanobis Euclidean² Distances

The cluster means for different characters revealed considerable genetic differences among the clones (Table 3). Cluster I had the highest mean values for vessel length (171.77), vessel diameter (223.11). However, the maximum mean value for wall

thickness was recorded in cluster VI (4.07), diameter at breast height in cluster V (1 186.50), height in cluster VII (22.67) and specific gravity in cluster III (0.69). Among different clusters, cluster I showed high mean performance for most of the characters. Hence the clones assembled in this cluster were not only divergent but were found with promising growth and wood parameters, which could easily be exploited for commercially.

In hybridization programme, selection of most divergent parents is utmost essential for the access of maximum heterosis in the shortest possible time. It could easily be done by selecting the parents from two divergent clusters. Clone 10 of cluster VII could be used in a variety of combinations. It is also important to obtain immediate gains of highly diverse clones by establishing them in the seed orchards.

Table 3. Cluster means for various characters of twelve clones of *Dalbergia sissoo*

Cluster	Characters						
No.	WT	VL	VD	FL	DBH	H	Sp.Gr
I	3.92	171.77	223.11	1003.83	1038.38	22.08	63.68
II	3.29	164.45	192.03	954.76	999	17.83	65.35
III	3.96	168.01	200.32	985.57	1100	22.5	69.09
IV	3.81	162.27	189.97	959.22	922	20.83	57.49
V	3.86	160.65	194.15	993.37	1186.5	21.33	57.26
VI	4.07	168.73	201.78	988.09	1115	18.67	62.74
VII	3.24	168.39	193.98	910.85	1038	22.67	62.76

Notes: WT, wall thickness; VL, vessel element length; VD, vessel element diameter; FL, fibre length; DBH, diameter at breast height; H, height; Sp.Gr, specific gravity.

Conclusion

Clonal forestry has mostly been alleged to offer narrow genetic base, yet vegetative propagation has strongly been recommended (Camphinhos and Ikemori 1980; Ahuja and Libby 1993). Adding a large number of intensively selected clones in the clone bank / trials and determining the diversity as well as genetic distance would immensely help to maintain genetically diverse population of high yielding clones. Using the planning stock from such gene bank, it is possible to develop a breeding programme with selective individuals of desired constitution. It is emphasized that clonal strategy should form a part of overall genetic improvement programme. However, the inadequate progress made in genetic improvement need not per se limit clonal strategy if the selection is carried out from diverse population by adopting proper tools and techniques so that genetically broad based productive clones are maintained (Gurumurthi et al. 1994).

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